SEQUENCE LISTING

<110> KAO CORPORATION

<120> Mutant Bacillus

<130> KS0816

<150> JP 2004-062852
<151> 2004.03.05

<160> 28

<170> PatentIn Ver. 3.1

<210> 1
<211> 371
<212> PRT
<213> Bacillus subtilis

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Glu Glu Ile Ala Glu Arg Met Ser Ser Phe Glu Ile Glu Ser Asp Gln
        35   40   45

Met Asp Glu Tyr Tyr Glu Phe Leu Gly Glu Gln Gly Val Glu Leu Ile
    50   55   60

Ser Glu Asn Glu Glu Thr Glu Asp Pro Asn Ile Gln Gln Leu Ala Lys
65   70   75   80

Ala Glu Glu Glu Phe Asp Leu Asn Asp Leu Ser Val Pro Pro Gly Val
                85   90   95

Lys Ile Asn Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Arg Val
                100   105   110

Asn Leu Leu Ser Ala Lys Glu Glu Ile Ala Tyr Ala Gln Lys Ile Glu
        115   120   125

Glu Gly Asp Glu Glu Ser Lys Arg Arg Leu Ala Glu Ala Asn Leu Arg
        130   135   140

Leu Val Val Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Met Leu Phe
145   150   155   160

Leu Asp Leu Ile His Glu Gly Asn Met Gly Leu Met Lys Ala Val Glu
                165   170   175

Lys Phe Asp Tyr Arg Lys Gly Tyr Lys Phe Ser Thr Tyr Ala Thr Trp
            180   185   190

Trp Ile Arg Gln Ala Ile Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr
            195   200   205

Ile Arg Ile Pro Val His Met Val Glu Thr Ile Asn Lys Leu Ile Arg
        210   215   220

Val Gln Arg Gln Leu Leu Gln Asp Leu Gly Arg Glu Pro Thr Pro Glu
225   230   235   240

Glu Ile Ala Glu Asp Met Asp Leu Thr Pro Glu Lys Val Arg Glu Ile
                245   250   255

Leu Lys Ile Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu
            260   265   270

Glu Asp Asp Ser His Leu Gly Asp Phe Ile Glu Asp Gln Glu Ala Thr
            275   280   285

Ser Pro Ser Asp His Ala Ala Tyr Glu Leu Leu Lys Glu Gln Leu Glu
        290   295   300

2

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Asp Val Leu Asp Thr Leu Thr Asp Arg Glu Glu Asn Val Leu Arg Leu
305             310             315             320


Arg Phe Gly Leu Asp Asp Gly Arg Thr Arg Thr Leu Glu Glu Val Gly
            325             330             335


Lys Val Phe Gly Val Thr Arg Glu Arg Ile Arg Gln Ile Glu Ala Lys
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Ala Leu Arg Lys Leu Arg His Pro Ser Arg Ser Lys Arg Leu Lys Asp
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Phe Leu Glu
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gctgacaaca acagtggcaa aagcttcaac aggagcaatt gagcacattc ctgtagcaag   180

agtcaccaat ttggcacgga cgttagaaga gatgaaagag cggggaatct gggttgtcgg   240

aacggatgcg tccgcgcgtg aggatttccg taatatggac ggcaatatgc ctttggctct   300

agtcatcgga agtgaaggaa aagggatggg ccgccttgtg aaggaaaagt gcgattttct   360

cattaaactc ccgatggccg gaaaggtaac ttcactaaat gcatctgtcg cggctggtct   420

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gaacagtttt gaagaggcga gagacgtact gattcagaaa atggcggaat atcaatcgta   600

tacaggaaac agggttattg ttgtttttga cgcgcatctc gtaaaagggc ttgagaaaaa   660

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3

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gatagaaaag ctcgctcagg ctttgaataa tattgcgact caaattcacg ttgcgacctc      780

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gcttctgaga gaggtagaaa cgattgaaag gcgaatagag agacgggtaa gaaaaatcac      900

ttccgaaaag ccggcgggta aaattgcttt atcggaagag gttttgaaaa cgtttgaaaa      960

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caaaatcaaa atgagtgata aggtccgtac aagcgagcat gcggcgtcaa tgggcggctc      180

acagatattc cttgagcccg gcgaagaaat gactgtcaaa gaaatgctga aaggcatcgc      240

aatcgcttcg ggaaatgacg cttccgtcgc catggctgaa tttatttccg gctctgaaga      300

agaatttgtg aagaaaatga ataaaaaagc aaaagagctg ggattgaaaa atacatcctt      360

taaaaaccca acaggactga ccgaggaagg acactacagc tctgcttatg acatggcaat      420

catggctaag gaattattga aatacgaatc aattacgaag tttaccggca cgtatgaaga      480

ttatctgcgt gaaaatacag ataaaaagtt ttggcttgta aatacaaatc gccttatcaa      540

attttatcct ggtgtagacg gcgtaaaaac aggctataca ggcgaagcga atattgtct       600

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gcctaaagaa agaaacgcgc aagtgacaaa aatgcttgac ttcgccttta gccaatatga      720

aacgcatcct ttatataaac gaaatcaaac agtagcaaaa gtaaaggtca aaaaagggaa      780

acaaaaattt atcgaactca ctacatctga gccgatttca atattgacga aaaaaggcga      840

ggatatgaac gatgtgaaaa aagaaatcaa gatgaaggac aatattagtg ctccgattca      900
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aaaaggccaa gagcttggca ctcttgttct gaaaaaggat ggagaagtac tcgctgaaag   960

tcctgttgct gcaaaagaag atatgaagaa agccgggttt atcacattct taaagcggac   1020

gatgggagac tggacaaaat ttaagtaatt atgccgaatg accactagtt ttgtcacggt   1080

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Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu
            20   25   30

Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
            35   40   45

Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
        50   55   60

Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met
65   70   75   80

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro
                85   90   95

Glu Leu Ile Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu
            100   105   110

Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
            115   120   125

5

Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile
    130   135   140

Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145   150   155   160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
            165   170   175

Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
            180   185   190

Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
        195   200   205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
    210   215   220

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225   230   235   240

Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly
            245   250   255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
            260   265   270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro
        275   280   285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
    290   295   300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
305   310   315   320

6

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Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp
            325                   330                   335


Pro Gly Pro Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly
            340                   345                   350


Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
            355                   360                   365


Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
        370                   375                   380


Gln Gly Phe Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala
385                   390                   395                   400


Val Asp Asn Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser
                405                   410                   415


Asn Asp Val Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala
            420                   425                   430


Asn Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr
            435                   440                   445


Met Asp Val Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile
        450                   455                   460


Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg
465                   470                   475                   480


Val Asn Ala Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala
                485                   490                   495


Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala
            500                   505                   510
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7

Phe His Glu Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly
    515   520   525

Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly
    530   535   540

Thr Glu Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val
545   550   555   560

Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala
      565   570   575

Gly Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly
      580   585   590

Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser
      595   600   605

Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu
    610   615   620

Val Arg Gly Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro
625   630   635   640

Val Arg Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro
      645   650   655

Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn
      660   665   670

Phe Asp Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr
      675   680   685

Glu Val Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr
    690   695   700

Leu Leu Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe

Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr
     725   730   735

Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro
    740   745   750

Pro Val Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys
    755   760   765

Glu Glu Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu
    770   775   780

Lys Lys Ala Val Lys Asn Glu Ala Lys Lys Lys
785   790   795

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gaaataaaag tagaagacaa aggacataag aaaattgcat tagtttttaat tatagaaaac 180

gccttttat aattatttat acctagaacg aaaatactgt ttcgaaagcg gtttactata   240

aaaccttata ttccggctct tttttaaaac aggggggtaaa aattcactct agtattctaa   300

tttcaacatg ctataataaa tttgtaagac gcaatatgca tctctttttt tacgatatat   360

gtaagcggtt aaccttgtgc tatatgccga tttaggaagg ggggtagatt gagtcaagta   420

gtaataatat agataactta taagttgttg agaagcagga gagcatctgg gttactcaca   480

agttttttta aaactttaac gaaagcactt tcggtaatgc ttatgaattt agctatttga   540

ttcaattact ttaaaaatat ttaggaggta at atg atg tta aga aag aaa aca   593
                                     Met Met Leu Arg Lys Lys Thr
                                                           -25

aag cag ttg att tct tcc att ctt att tta gtt tta ctt cta tct tta   641
Lys Gln Leu Ile Ser Ser Ile Leu Ile Leu Val Leu Leu Leu Ser Leu
        -20   -15   -10

ttt ccg gca gct ctt gca gca gaa gga aac act cgt gaa gac aat ttt   689
Phe Pro Ala Ala Leu Ala Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe
    -5   -1 1   5   10

aaa cat tta tta ggt aat gac aat gtt aaa cgc cct tct gag gct ggc   737
Lys His Leu Leu Gly Asn Asp Asn Val Lys Arg Pro Ser Glu Ala Gly
                15   20   25

gca tta caa tta caa gaa gtc gat gga caa atg aca tta gta gat caa   785
Ala Leu Gln Leu Gln Glu Val Asp Gly Gln Met Thr Leu Val Asp Gln
            30   35   40

cat gga gaa aaa att caa tta cgt gga atg agt aca cac gga tta cag   833
His Gly Glu Lys Ile Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln
        45   50   55

tgg ttt cct gag atc ttg aat gat aac gca tac aaa gct ctt tct aac   881
Trp Phe Pro Glu Ile Leu Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn
    60   65   70

gat tgg gat tcc aat atg att cgt ctt gct atg tat gta ggt gaa aat   929
Asp Trp Asp Ser Asn Met Ile Arg Leu Ala Met Tyr Val Gly Glu Asn
75   80   85   90

ggg tac gct aca aac cct gag tta atc aaa caa aga gtg att gat gga   977
Gly Tyr Ala Thr Asn Pro Glu Leu Ile Lys Gln Arg Val Ile Asp Gly
            95   100   105

10

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att gag tta gcg att gaa aat gac atg tat gtt att gtt gac tgg cat        1025
Ile Glu Leu Ala Ile Glu Asn Asp Met Tyr Val Ile Val Asp Trp His
            110                 115                 120

gtt cat gcg cca ggt gat cct aga gat cct gtt tat gca ggt gct aaa        1073
Val His Ala Pro Gly Asp Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys
            125                 130                 135

gat ttc ttt aga gaa att gca gct tta tac cct aat aat cca cac att        1121
Asp Phe Phe Arg Glu Ile Ala Ala Leu Tyr Pro Asn Asn Pro His Ile
            140                 145                 150

att tat gag tta gcg aat gag ccg agt agt aat aat aat ggt gga gca        1169
Ile Tyr Glu Leu Ala Asn Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala
155                 160                 165                 170

ggg att ccg aat aac gaa gaa ggt tgg aaa gcg gta aaa gaa tat gct        1217
Gly Ile Pro Asn Asn Glu Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala
            175                 180                 185

gat cca att gta gaa atg tta cgt aaa agc ggt aat gca gat gac aac        1265
Asp Pro Ile Val Glu Met Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn
            190                 195                 200

att atc att gtt ggt agt cca aac tgg agt cag cgt ccg gac tta gca        1313
Ile Ile Ile Val Gly Ser Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala
            205                 210                 215

gct gat aat cca att gat gat cac cat aca atg tat act gtt cac ttc        1361
Ala Asp Asn Pro Ile Asp Asp His His Thr Met Tyr Thr Val His Phe
            220                 225                 230

tac act ggt tca cat gct gct tca act gaa agc tat ccg tct gaa act        1409
Tyr Thr Gly Ser His Ala Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr
235                 240                 245                 250

cct aac tct gaa aga gga aac gta atg agt aac act cgt tat gcg tta        1457
Pro Asn Ser Glu Arg Gly Asn Val Met Ser Asn Thr Arg Tyr Ala Leu
            255                 260                 265

gaa aac gga gta gcg gta ttt gca aca gag tgg gga acg agt caa gct        1505
Glu Asn Gly Val Ala Val Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala
            270                 275                 280

agt gga gac ggt ggt cct tac ttt gat gaa gca gat gta tgg att gaa        1553
Ser Gly Asp Gly Gly Pro Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu
            285                 290                 295

ttt tta aat gaa aac aac att agc tgg gct aac tgg tct tta acg aat        1601
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11

Phe Leu Asn Glu Asn Asn Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn
    300   305   310

aaa aat gaa gta tct ggt gca ttt aca cca ttc gag tta ggt aag tct   1649
Lys Asn Glu Val Ser Gly Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser
315   320   325   330

aac gca acc aat ctt gac cca ggt cca gat cat gtg tgg gca cca gaa   1697
Asn Ala Thr Asn Leu Asp Pro Gly Pro Asp His Val Trp Ala Pro Glu
                335   340   345

gaa tta agt ctt tct gga gaa tat gta cgt gct cgt att aaa ggt gtg   1745
Glu Leu Ser Leu Ser Gly Glu Tyr Val Arg Ala Arg Ile Lys Gly Val
                350   355   360

aac tat gag cca atc gac cgt aca aaa tac acg aaa gta ctt tgg gac   1793
Asn Tyr Glu Pro Ile Asp Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp
            365   370   375

ttt aat gat gga acg aag caa gga ttt gga gtg aat tcg gat tct cca   1841
Phe Asn Asp Gly Thr Lys Gln Gly Phe Gly Val Asn Ser Asp Ser Pro
        380   385   390

aat aaa gaa ctt att gca gtt gat aat gaa aac aac act ttg aaa gtt   1889
Asn Lys Glu Leu Ile Ala Val Asp Asn Glu Asn Asn Thr Leu Lys Val
395   400   405   410

tcg gga tta gat gta agt aac gat gtt tca gat ggc aac ttc tgg gct   1937
Ser Gly Leu Asp Val Ser Asn Asp Val Ser Asp Gly Asn Phe Trp Ala
                415   420   425

aat gct cgt ctt tct gcc aac ggt tgg gga aaa agt gtt gat att tta   1985
Asn Ala Arg Leu Ser Ala Asn Gly Trp Gly Lys Ser Val Asp Ile Leu
                430   435   440

ggt gct gag aag ctt aca atg gat gtt att gtt gat gaa cca acg acg   2033
Gly Ala Glu Lys Leu Thr Met Asp Val Ile Val Asp Glu Pro Thr Thr
                445   450   455

gta gct att gcg gcg att cca caa agt agt aaa agt gga tgg gca aat   2081
Val Ala Ile Ala Ala Ile Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn
        460   465   470

cca gag cgt gct gtt cga gtg aac gcg gaa gat ttt gtc cag caa acg   2129
Pro Glu Arg Ala Val Arg Val Asn Ala Glu Asp Phe Val Gln Gln Thr
475   480   485   490

gac ggt aag tat aaa gct gga tta aca att aca gga gaa gat gct cct   2177
Asp Gly Lys Tyr Lys Ala Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro

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aac cta aaa aat atc gct ttt cat gaa gaa gat aac aat atg aac aac        2225
Asn Leu Lys Asn Ile Ala Phe His Glu Glu Asp Asn Asn Met Asn Asn
        510                 515                 520

atc att ctg ttc gtg gga act gat gca gct gac gtt att tac tta gat        2273
Ile Ile Leu Phe Val Gly Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp
        525                 530                 535

aac att aaa gta att gga aca gaa gtt gaa att cca gtt gtt cat gat        2321
Asn Ile Lys Val Ile Gly Thr Glu Val Glu Ile Pro Val Val His Asp
    540                 545                 550

cca aaa gga gaa gct gtt ctt cct tct gtt ttt gaa gac ggt aca cgt        2369
Pro Lys Gly Glu Ala Val Leu Pro Ser Val Phe Glu Asp Gly Thr Arg
555                 560                 565                 570

caa ggt tgg gac tgg gct gga gag tct ggt gtg aaa aca gct tta aca        2417
Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val Lys Thr Ala Leu Thr
                575                 580                 585

att gaa gaa gca aac ggt tct aac gcg tta tca tgg gaa ttt gga tat        2465
Ile Glu Glu Ala Asn Gly Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr
                590                 595                 600

cca gaa gta aaa cct agt gat aac tgg gca aca gct cca cgt tta gat        2513
Pro Glu Val Lys Pro Ser Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp
                605                 610                 615

ttc tgg aaa tct gac ttg gtt cgc ggt gag aat gat tat gta gct ttt        2561
Phe Trp Lys Ser Asp Leu Val Arg Gly Glu Asn Asp Tyr Val Ala Phe
        620                 625                 630

gat ttc tat cta gat cca gtt cgt gca aca gaa ggc gca atg aat atc        2609
Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu Gly Ala Met Asn Ile
635                 640                 645                 650

aat tta gta ttc cag cca cct act aac ggg tat tgg gta caa gca cca        2657
Asn Leu Val Phe Gln Pro Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro
                655                 660                 665

aaa acg tat acg att aac ttt gat gaa tta gag gaa gcg aat caa gta        2705
Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu Glu Ala Asn Gln Val
                670                 675                 680

aat ggt tta tat cac tat gaa gtg aaa att aac gta aga gat att aca        2753
Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn Val Arg Asp Ile Thr
                685                 690                 695
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aac att caa gat gac acg tta cta cgt aac atg atg atc att ttt gca      2801
Asn Ile Gln Asp Asp Thr Leu Leu Arg Asn Met Met Ile Ile Phe Ala
    700                 705             710

gat gta gaa agt gac ttt gca ggg aga gtc ttt gta gat aat gtt cgt      2849
Asp Val Glu Ser Asp Phe Ala Gly Arg Val Phe Val Asp Asn Val Arg
715             720             725             730

ttt gag ggg gct gct act act gag ccg gtt gaa cca gag cca gtt gat      2897
Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu Pro Glu Pro Val Asp
                735             740             745

cct ggc gaa gag acg cca cct gtc gat gag aag gaa gcg aaa aaa gaa      2945
Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys Glu Ala Lys Lys Glu
                750             755             760

caa aaa gaa gca gag aaa gaa gag aaa gaa gca gta aaa gaa gaa aag      2993
Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala Val Lys Glu Glu Lys
                765             770             775

aaa gaa gct aaa gaa gaa aag aaa gca gtc aaa aat gag gct aag aaa      3041
Lys Glu Ala Lys Glu Glu Lys Lys Ala Val Lys Asn Glu Ala Lys Lys
    780             785             790

aaa taatctatta aactagttat agggttatct aaaggtctga tgtagatctt           3094
Lys
795

ttagataacc tttttcttgc ataactggac acagagttgt tattaaagaa agtaag        3150
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<210> 6
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Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
        35              40              45
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14

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Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
    50                55                60

Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met
65                  70              75                  80

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro
                85              90                  95

Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu
            100             105             110

Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
        115             120             125

Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile
    130             135             140

Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145             150             155             160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
            165             170             175

Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
            180             185             190

Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
        195             200             205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
    210             215             220

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225             230             235             240
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15

Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
           245   250   255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
           260   265   270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro
           275   280   285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
           290   295   300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
305   310   315   320

Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp
           325   330   335

Pro Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly
           340   345   350

Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
           355   360   365

Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
           370   375   380

Gln Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile
385   390   395   400

Glu Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn
           405   410   415

Asp Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp
           420   425   430

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Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met
    435               440              445

Asp Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro
    450               455              460

Gln Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val
465               470              475              480

Glu Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu
            485              490              495

Thr Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His
        500              505              510

Ala Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu
        515              520              525

Gly Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu
    530              535              540

Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro
545               550              555              560

Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu
            565              570              575

Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn
        580              585              590

Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn
        595              600              605

Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg
    610              615              620

Gly Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg
```

Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr
            645   650   655

Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp
            660   665   670

Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val
            675   680   685

Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu
            690   695   700

Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly
705   710   715   720

Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu
            725   730   735

Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val
            740   745   750

Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu
            755   760   765

Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys
            770   775   780

Ala Ile Lys Asn Glu Ala Thr Lys Lys
785   790

<210> 7
<211> 3332
<212> DNA
<213> Bacillus sp. KSM-64

<220>

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<222> (610)..(3075)
<223>

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<223>

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<223>

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agtacttacc attttagagt caaaagatag aagccaagca ggatttgccg atgcaaccgg   60

cttatattta gagggaattt cttttttaaat tgaatacgga ataaaatcag gtaaacaggt   120

cctgatttta ttttttttgaa ttttttttgag aactaaagat tgaaatagaa gtagaagaca   180

acggacataa gaaaattgta ttagtttttaa ttatagaaaa cgcttttcta taattattta   240

tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaccttat attccggctc   300

ttttttttaaa cagggggtga aaattcactc tagtattcta atttcaacat gctataataa   360

atttgtaaga cgcaatatac atctttttttt tatgatattt gtaagcggtt aaccttgtgc   420

tatatgccga tttaggaagg gggtagattg agtcaagtag tcataattta gataacttat   . ,480

aagttgttga gaagcaggag agaatctggg ttactcacaa gttttttaaa acattatcga   540

aagcactttc ggttatgctt atgaatttag ctatttgatt caattacttt aataatttta   600

ggaggtaat atg atg tta aga aag aaa aca aag cag ttg att tct tcc att   651
         Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile
             -25   -20

ctt att tta gtt tta ctt cta tct tta ttt ccg aca gct ctt gca gca   699
Leu Ile Leu Val Leu Leu Leu Ser Leu Phe Pro Thr Ala Leu Ala Ala
-15   -10   -5   -1 1

gaa gga aac act cgt gaa gac aat ttt aaa cat tta tta ggt aat gac   747
Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp
        5   10   15

aat gtt aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa gtc   795
Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val

19

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gat gga caa atg aca tta gta gat caa cat gga gaa aaa att caa tta        843
Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu
    35              40              45

cgt gga atg agt aca cac gga tta caa tgg ttt cct gag atc ttg aat        891
Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn
50              55              60              65

gat aac gca tac aaa gct ctt gct aac gat tgg gaa tca aat atg att        939
Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile
                70              75              80

cgt cta gct atg tat gtc ggt gaa aat ggc tat gct tca aat cca gag        987
Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu
            85              90              95

tta att aaa agc aga gtc att aaa gga ata gat ctt gct att gaa aat       1035
Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn
        100             105             110

gac atg tat gtc atc gtt gat tgg cat gta cat gca cct ggt gat cct       1083
Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro
    115             120             125

aga gat ccc gtt tac gct gga gca gaa gat ttc ttt aga gat att gca       1131
Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile Ala
130             135             140             145

gca tta tat cct aac aat cca cac att att tat gag tta gcg aat gag       1179
Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu
            150             155             160

cca agt agt aac aat aat ggt gga gct ggg att cca aat aat gaa gaa       1227
Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu
            165             170             175

ggt tgg aat gcg gta aaa gaa tac gct gat cca att gta gaa atg tta       1275
Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu
            180             185             190

cgt gat agc ggg aac gca gat gac aat att atc att gtg ggt agt cca       1323
Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro
    195             200             205

aac tgg agt cag cgt cct gac tta gca gct gat aat cca att gat gat       1371
Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp
210             215             220             225
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cac cat aca atg tat act gtt cac ttc tac act ggt tca cat gct gct      1419
His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala
                230                 235                 240

tca act gaa agc tat ccg cct gaa act cct aac tct gaa aga gga aac      1467
Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly Asn
                245                 250                 255

gta atg agt aac act cgt tat gcg tta gaa aac gga gta gca gta ttt      1515
Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe
                260                 265                 270

gca aca gag tgg gga act agc caa gca aat gga gat ggt ggt cct tac      1563
Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro Tyr
                275                 280                 285

ttt gat gaa gca gat gta tgg att gag ttt tta aat gaa aac aac att      1611
Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile
290                 295                 300                 305

agc tgg gct aac tgg tct tta acg aat aaa aat gaa gta tct ggt gca      1659
Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala
                310                 315                 320

ttt aca cca ttc gag tta ggt aag tct aac gca aca agt ctt gac cca      1707
Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp Pro
                325                 330                 335

ggg cca gac caa gta tgg gta cca gaa gag tta agt ctt tct gga gaa      1755
Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly Glu
                340                 345                 350

tat gta cgt gct cgt att aaa ggt gtg aac tat gag cca atc gac cgt      1803
Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg
                355                 360                 365

aca aaa tac acg aaa gta ctt tgg gac ttt aat gat gga acg aag caa      1851
Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln
370                 375                 380                 385

gga ttt gga gtg aat gga gat tct cca gtt gaa gat gta gtt att gag      1899
Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile Glu
                390                 395                 400

aat gaa gcg ggc gct tta aaa ctt tca gga tta gat gca agt aat gat      1947
Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn Asp
                405                 410                 415
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21

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gtt tct gaa ggt aat tac tgg gct aat gct cgt ctt tct gcc gac ggt      1995
Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp Gly
        420               425               430

tgg gga aaa agt gtt gat att tta ggt gct gaa aaa ctt act atg gat      2043
Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp
        435               440               445

gtg att gtt gat gag ccg acc acg gta tca att gct gca att cca caa      2091
Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro Gln
450               455               460               465

ggg cca tca gcc aat tgg gtt aat cca aat cgt gca att aag gtt gag      2139
Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val Glu
                470               475               480

cca act aat ttc gta ccg tta gga gat aag ttt aaa gcg gaa tta act      2187
Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu Thr
                485               490               495

ata act tca gct gac tct cca tcg tta gaa gct att gcg atg cat gct      2235
Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His Ala
        500               505               510

gaa aat aac aac atc aac aac atc att ctt ttt gta gga act gaa ggt      2283
Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu Gly
        515               520               525

gct gat gtt atc tat tta gat aac att aaa gta att gga aca gaa gtt      2331
Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val
530               535               540               545

gaa att cca gtt gtt cat gat cca aaa gga gaa gct gtt ctt cct tct      2379
Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser
                550               555               560

gtt ttt gaa gac ggt aca cgt caa ggt tgg gac tgg gct gga gag tct      2427
Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser
                565               570               575

ggt gtg aaa aca gct tta aca att gaa gaa gca aac ggt tct aac gcg      2475
Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala
        580               585               590

tta tca tgg gaa ttt gga tac cca gaa gta aaa cct agt gat aac tgg      2523
Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp
        595               600               605

gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg gtt cgc ggt      2571
```

22

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Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly
610             615             620             625

gaa aat gat tat gta act ttt gat ttc tat cta gat cca gtt cgt gca    2619
Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala
                630             635             640

aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac    2667
Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn
                645             650             655

ggg tat tgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa    2715
Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu
            660             665             670

tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa    2763
Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys
        675             680             685

att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt    2811
Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg
690             695             700             705

aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga    2859
Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg
                710             715             720

gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg    2907
Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro
            725             730             735

gtt gaa cca gag cca gtt gat cct ggc gaa gag acg ccg cct gtc gat    2955
Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp
        740             745             750

gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa    3003
Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys
    755             760             765

gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca    3051
Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala
770             775             780             785

atc aaa aat gag gct acg aaa aaa taatctaata aactagttat agggttatct   3105
Ile Lys Asn Glu Ala Thr Lys Lys
                790

aaaggtctga tgcagatctt ttagataacc ttttttttgca taactggaca tagaatggtt   3165


                                    23
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attaaagaaa gcaaggtgtt tatacgatat taaaaaggta gcgattttaa attgaaacct   3225

ttaataatgt cttgtgatag aatgatgaag taatttaaga gggggaaacg aagtgaaaac   3285

ggaaatttct agtagaagaa aaacagacca agaaatactg caagctt   3332

<210> 8
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
      f sigA in Bacillus subtilis

<400> 8
atggctgata aacaaaccca 20

<210> 9
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
      f sigA in Bacillus subtilis

<400> 9
caccacaatg ttcatttgca 20

<210> 10
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
      f the upstream region of sigH in Bacillus subtilis

<400> 10
acagcctttc ttcctcattc t 21

<210> 11
<211> 42
<212> DNA

24

<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucle
otide sequence of the upstream region of sigH in Bacillus subtili
s and its 5'-portion designed from nucleotide sequence of sigA in
Bacillus subtilis

<400> 11
cgtgggtttg tttatcagcc attccgatcc ccccggcgca cg 42

<210> 12
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
f the upstream region of sigF in Bacillus subtilis

<400> 12
gctgatagaa cgtgacacgg g 21

<210> 13
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucle
otide sequence of the upstream region of sigF in Bacillus subtili
s and its 5'-portion designed from nucleotide sequence of sigA in
Bacillus subtilis

<400> 13
cgtgggtttg tttatcagcc atgctcattc ctccttgata tg 42

<210> 14
<211> 19
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
f plasmid pC194

<400> 14
caactaaagc acccattag 19

<210> 15
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucle
      otide sequence of plasmid pC194 and its 5'-portion designed from
      nucleotide sequence of sigA in Bacillus subtilis

<400> 15
catttgcaaa tgaacattgt ggtgcttctt caactaacgg ggca 44

<210> 16
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
      f sigA in Bacillus subtilis; the sequence containing a nucleotide
       substitution for destroying the initiation codon of sigA

<400> 16
atagctgata aacaaaccca 20

<210> 17
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucle
      otide sequence of the upstream region of sigF in Bacillus subtili
      s and its 5'-portion designed from nucleotide sequence of sigA in
       Bacillus subtilis; the sequence containing a nucleotide substitu
      tion for destroying the initiation codon of sigA

<400> 17
cgtgggtttg tttatcagct atgctcattc ctccttgata tg 42

<210> 18

26

<211> 1795
<212> DNA
<213> Bacillus sp. KSM-K38

<220>
<221> CDS
<222> (212)..(1714)
<223>

<220>
<221> sig_peptide
<222> (212)..(274)
<223>

<220>
<221> mat_peptide
<222> (275)..(1714)
<223>

<400> 18

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caggccagcc aaagtagcca ccaactaagt aacatcgatt caggataaaa gtatgcgaaa        60

cgatgcgcaa aactgcgcaa ctactagcac tcttcaggga ctaaaccacc tttttttccaa       120

aaatgacatc atataaacaa atttgtctac caatcactat ttaaagctgt ttatgatata       180

tgtaagcgtt atcattaaaa ggaggtattt g atg aga aga tgg gta gta gca          232
                                   Met Arg Arg Trp Val Val Ala
                                   -20              -15

atg ttg gca gtg tta ttt tta ttt cct tcg gta gta gtt gca gat gga        280
Met Leu Ala Val Leu Phe Leu Phe Pro Ser Val Val Val Ala Asp Gly
        -10              -5              -1   1

ttg aac ggt acg atg atg cag tat tat gag tgg cat ttg gaa aac gac        328
Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp
        5                10               15

ggg cag cat tgg aat cgg ttg cac gat gat gcc gca gct ttg agt gat        376
Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu Ser Asp
    20               25               30

gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt aat agt        424
Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser
35               40               45               50

cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag        472
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
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ttc aat caa aag ggt act gtt cga acg aaa tac gga act aag gca cag      520
Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln
             70              75              80

ctt gaa cga gct att ggg tcc ctt aaa tct aat gat atc aat gta tac      568
Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn Val Tyr
         85              90              95

gga gat gtc gtg atg aat cat aaa atg gga gct gat ttt acg gag gca      616
Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr Glu Ala
    100             105             110

gtg caa gct gtt caa gta aat cca acg aat cgt tgg cag gat att tca      664
Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp Ile Ser
115             120             125             130

ggt gcc tac acg att gat gcg tgg acg ggt ttc gac ttt tca ggg cgt      712
Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser Gly Arg
             135             140             145

aac aac gcc tat tca gat ttt aag tgg aga tgg ttc cat ttt aat ggt      760
Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe Asn Gly
             150             155             160

gtt gac tgg gat cag cgc tat caa gaa aat cat att ttc cgc ttt gca      808
Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg Phe Ala
             165             170             175

aat acg aac tgg aac tgg cga gtg gat gaa gag aac ggt aat tat gat      856
Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn Tyr Asp
    180             185             190

tac ctg tta gga tcg aat atc gac ttt agt cat cca gaa gta caa gat      904
Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val Gln Asp
195             200             205             210

gag ttg aag gat tgg ggt agc tgg ttt acc gat gag tta gat ttg gat      952
Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp Leu Asp
             215             220             225

ggt tat cgt tta gat gct att aaa cat att cca ttc tgg tat aca tct      1000
Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr Thr Ser
             230             235             240

gat tgg gtt cgg cat cag cgc aac gaa gca gat caa gat tta ttt gtc      1048
Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu Phe Val
             245             250             255
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gta ggg gaa tat tgg aag gat gac gta ggt gct ctc gaa ttt tat tta   1096
Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe Tyr Leu
    260   265   270

gat gaa atg aat tgg gag atg tct cta ttc gat gtt cca ctt aat tat   1144
Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu Asn Tyr
275   280   285   290

aat ttt tac cgg gct tca caa caa ggt gga agc tat gat atg cgt aat   1192
Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met Arg Asn
                  295   300   305

att tta cga gga tct tta gta gaa gcg cat ccg atg cat gca gtt acg   1240
Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala Val Thr
              310   315   320

ttt gtt gat aat cat gat act cag cca ggg gag tca tta gag tca tgg   1288
Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu Ser Trp
          325   330   335

gtt gct gat tgg ttt aag cca ctt gct tat gcg aca att ttg acg cgt   1336
Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu Thr Arg
    340   345   350

gaa ggt ggt tat cca aat gta ttt tac ggt gat tac tat ggg att cct   1384
Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro
355   360   365   370

aac gat aac att tca gct aaa aaa gat atg att gat gag ctg ctt gat   1432
Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu Leu Asp
              375   380   385

gca cgt caa aat tac gca tat ggc acg cag cat gac tat ttt gat cat   1480
Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His
              390   395   400

tgg gat gtt gta gga tgg act agg gaa gga tct tcc tcc aga cct aat   1528
Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg Pro Asn
          405   410   415

tca ggc ctt gcg act att atg tcg aat gga cct ggt ggt tcc aag tgg   1576
Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser Lys Trp
    420   425   430

atg tat gta gga cgt cag aat gca gga caa aca tgg aca gat tta act   1624
Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp Leu Thr
435   440   445   450

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ggt aat aac gga gcg tcc gtt aca att aat ggc gat gga tgg ggc gaa      1672
Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp Gly Glu
            455                 460                 465

ttc ttt acg aat gga gga tct gta tcc gtg tac gtg aac caa taacaaaaa   1723
Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
            470                 475                 480

gccttgagaa gggattcctc cctaactcaa ggctttcttt atgtcgctta gctttacgct   1783

tctacgactt tg                                                        1795


<210>  19
<211>  480
<212>  PRT
<213>  Bacillus sp. KSM-K38

<400>  19

Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
1                 5                 10                  15


Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
            20                  25                  30


Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
        35                  40                  45


Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
        50                  55                  60


Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65                  70                  75                  80


Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
                85                  90                  95


Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
            100                 105                 110


Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
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30

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
      130   135   140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145   150   155   160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
                165   170   175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
              180   185   190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
          195   200   205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
    210   215   220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225   230   235   240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
              245   250   255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
              260   265   270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
          275   280   285

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
          290   295   300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305   310   315   320

31

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
            325   330   335

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
            340   345   350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
            355   360   365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
    370   375   380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385   390   395   400

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
            405   410   415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
            420   425   430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
            435   440   445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
    450   455   460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465   470   475   480

<210> 20
<211> 1441
<212> DNA
<213> Bacillus clausii KSM-K16

<220>
<221> CDS

32

<222> (164)..(1303)
<223>

<400> 20
tggtagcttt ccccacttga aaccgttta atcaaaaaac aaagtgggaa aattctgtta   60

acttaatgtt aataattgtt tcccaatagg caaatctttc taactttgat acgtttaaac   120

taccagcttg gacgagttgg gataaaagtg aggagggaac cga atg aag aaa ccg   175
                                                    Met Lys Lys Pro
                                                    1

ttg ggg aaa att gtc gca agc acc gca cta ctc att tct gtt gct ttt   223
Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile Ser Val Ala Phe
5   10   15   20

agt tca tcg atc gca tcg gct gct gag gaa gca aaa gaa aaa tat tta   271
Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala Lys Glu Lys Tyr Leu
             25   30   35

att ggc ttt aat gag cag gaa gca gtt agt gag ttt gta gag caa ata   319
Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu Phe Val Glu Gln Ile
              40   45   50

gag gca aat gac gat gtc gcg att ctc tct gag gaa gag gaa gtc gaa   367
Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu Glu Glu Val Glu
             55   60   65

att gaa ttg ctt cat gag ttt gaa acg att cct gtt tta tct gtt gag   415
Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val Leu Ser Val Glu
           70   75   80

tta agt cca gaa gat gtg gac gcg ctt gag ctc gat cca acg att tcg   463
Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp Pro Thr Ile Ser
85   90   95   100

tat att gaa gag gat gca gaa gta acg aca atg gcg caa tca gtg cca   511
Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala Gln Ser Val Pro
                 105   110   115

tgg gga att agc cgt gta caa gcc cca gct gcc cat aac cgt gga ttg   559
Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala His Asn Arg Gly Leu
             120   125   130

aca ggt tct ggt gta aaa gtt gct gtc ctc gat acg ggt att tcc acc   607
Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp Thr Gly Ile Ser Thr
             135   140   145

cat cca gac tta aat att cgc ggt ggt gct agc ttt gtg cca gga gaa   655

33

```
His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser Phe Val Pro Gly Glu
    150             155             160


cca tcc act caa gat gga aat gga cat ggc acg cat gtg gca ggg acg      703
Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr His Val Ala Gly Thr
165             170             175             180


att gct gct tta aac aat tcg att ggc gtt ctg ggc gta gca ccg agc      751
Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser
                185             190             195


gcg gaa cta tac gct gta aaa gta tta ggc gcg agc ggt tca ggt tcg      799
Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala Ser Gly Ser Gly Ser
                200             205             210


gtc agc tcg att gcc caa gga ttg gaa tgg gca ggg aac aat ggc atg      847
Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala Gly Asn Asn Gly Met
        215             220             225


cac gtt gcg aat ttg agt tta gga agc ccg tcg ccg agt gca aca ctt      895
His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser Pro Ser Ala Thr Leu
    230             235             240


gag caa gct gtt aat agc gct act tct aga ggc gtt ctt gtc gta gca      943
Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly Val Leu Val Val Ala
245             250             255             260


gca tct ggt aat tca ggt gca ggc tca atc agc tat ccg gcc cgt tat      991
Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr Pro Ala Arg Tyr
                265             270             275


gcg aac gca atg gca gtc gga gcg act gac caa aac aac aac cgc gct     1039
Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln Asn Asn Asn Arg Ala
                280             285             290


agc ttt tca cag tat gga gct ggg ctt gac att gtc gcg cca ggt gtc     1087
Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val Ala Pro Gly Val
                295             300             305


aat gtg cag agc aca tac cca ggt tca aca tat gcc agc tta aac ggt     1135
Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala Ser Leu Asn Gly
        310             315             320


aca tcg atg gct act cct cat gtt gca ggt gta gca gcc ctt gtt aaa     1183
Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala Ala Leu Val Lys
325             330             335             340


caa aag aat cca tct tgg tcc aat gta caa atc cgc aat cat cta aag     1231
Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg Asn His Leu Lys
```

34

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aat acg gca acg ggt tta gga aac acg aac ttg tat gga agc ggg ctt    1279
Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr Gly Ser Gly Leu
        360                 365                 370

gtc aat gca gaa gcg gca aca cgc taatcaataa taataacgct gtgtgcttta    1333
Val Asn Ala Glu Ala Ala Thr Arg
        375                 380

agcacacagc gttttttagt gtgtatgaat cgaaaaagag aaatagatcg ctgatttcaa    1393

aaagcgagcg taaagggcta ttgaagctct ttacgcttgc aggatttg               1441
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<210> 21
<211> 380
<212> PRT
<213> Bacillus clausii KSM-K16

<400> 21

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Met Lys Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile
1               5                   10                  15


Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala Lys
            20                  25                  30


Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu Phe
        35                  40                  45


Val Glu Gln Ile Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu
    50                  55                  60


Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val
65                  70                  75                  80


Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp
            85                  90                  95


Pro Thr Ile Ser Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala
            100                 105                 110
```

Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala His
        115   120   125

Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp Thr
        130   135   140

Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser Phe
145   150   155   160

Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr His
                165   170   175

Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly
            180   185   190

Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala Ser
            195   200   205

Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala Gly
    210   215   220

Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser Pro
225   230   235   240

Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly Val
                245   250   255

Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr
            260   265   270

Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln Asn
        275   280   285

Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val
        290   295   300

Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala
305   310   315   320

Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala
                325   330   335

Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg
            340   345   350

Asn His Leu Lys Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr
        355   360   365

Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
    370   375   380

<210> 22
<211> 46
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucle
      otide sequence of the alkaline protease gene in Bacillus clausii
      KSM-K16 and its 5'-portion designed from nucleotide sequence of t
      he upstream region of the alkaline cellulase gene in Bacillus sp.
      KSM-S237

<400> 22
actttaaaaa tatttaggag gtaatatgaa gaaaccgttg gggaaa   46

<210> 23
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
      f the downstream region of the alkaline protease gene in Bacillus
       clausii KSM-K16 with a insertion of the BglII restriction site a
      t the 5'-end

<400> 23
gggagatctt cagcgatcta tttctctttt tc   32

<210> 24
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
f the upstream region of the alkaline cellulase gene in Bacillus
sp. KSM-S237 with a insertion of the BamHI restriction site at th
e 5'-end

<400> 24
cccggatcca acaggcttat attta   25

<210> 25
<211> 46
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucle
otide sequence of the upstream region of the alkaline cellulase g
ene in Bacillus sp. KSM-S237 and its 5'-portion designed from nuc
leotide sequence of the alkaline protease gene in Bacillus clausi
i KSM-K16

<400> 25
tttccccaac ggtttcttca tattacctcc taaatatttt taaagt   46

<210> 26
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucle
otide sequence of the alkaline amylase gene in Bacillus sp. KSM-K
38 and its 5'-portion designed from nucleotide sequence of the al
kaline cellulase gene in Bacillus sp. KSM-S237

<400> 26
gctcttgcag cagatggatt gaacggtacg   30

<210> 27
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
f the downstream region of the alkaline amylase gene in Bacillus
sp. KSM-K38 with a insertion of the XbaI restriction site at the
5'-end

<400> 27
ttggtctaga ccccaagctt caaagtcgta   30

<210> 28
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucle
otide sequence of the alkaline cellulase gene in Bacillus sp. KSM
-S237 and its 5'-portion designed from nucleotide sequence of the
alkaline amylase gene in Bacillus sp. KSM-K38

<400> 28
ttcaatccat ctgctgcaag agctgccgg   29